

ABSTRACT

[0094] A method for transcript analysis in which multiple polynucleotides are derived from a multiplicity of mRNAs derived from a biological sample, with the polynucleotides having homology to at least one known reference sequence, and expressing and assessing the polypeptides. The assessment of the polypeptides focuses on at least one physical property of the polypeptides to enable determination of their sequences, sometimes with reference to one or more known reference sequences.